





OTPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/995,898A

DATE: 05/02/2002 TIME: 17:22:38

Input Set : A:\00-108.txt

Output Set: N:\CRF3\05022002\1995898A.raw

4 <110> APPLICANT: Presnell, Scott R. Xu, Wenfeng 5 Novak, Julia E. Whitmore, Theodore E. Grant, Francis J. 10 <120> TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19 13 <130> FILE REFERENCE: 00-108 C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/995,898A C--> 15 <141> CURRENT FILING DATE: 2001-11-28 15 <150> PRIOR APPLICATION NUMBER: US 60/253,561 16 <151> PRIOR FILING DATE: 2000-11-28 18 <150> PRIOR APPLICATION NUMBER: US 60/267,211 19 <151> PRIOR FILING DATE: 2001-02-07 21 <160> NUMBER OF SEQ ID NOS: 50 23 <170> SOFTWARE: FastSEQ for Windows Version 3.0 25 <210> SEO ID NO: 1 26 <211> LENGTH: 1476 27 <212> TYPE: DNA 28 <213> ORGANISM: Homo sapiens 30 <220> FEATURE: 31 <221> NAME/KEY: CDS 32 <222> LOCATION: (1)...(1473) 34 <400> SEQUENCE: 1 atg gcg ggg ccc gag cgc tgg ggc ccc ctg ctc ctg tgc ctg cag 48 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Cys Leu Leu Gln 10 37 96 gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg 39 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu 40 25 ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc 144 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly 44 40 35 45 aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc 192 47 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr 48 49 cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg 240 51 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu 52 70 53 cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc 288 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe 56 90 85 57 aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg 336

Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val

ENTERED

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Input Set : A:\00-108.txt

Output Set: N:\CRF3\05022002\1995898A.raw

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65			115			cag	200		aaa	ato	cta	ant		aat	acc	aca	432
67	gtc	ctg	gtg	CLC	mb	Gln	mhr	Clu	Clu	Tla	T.AII	Ser	Δla	Agn	Ala	Thr	
68	vaı		vaı	Leu	Thr	GIII	135	GIU	GIU	116	Deu	140	AIU	AJII	713.0	1111	
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76	Ата	Pne	Trp	GIY		СТА	Ald	СТУ	1111	170	1111	пеа	riic	110	175		
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84	HlS	His		Leu	ser	Ald	Arg	200	TIE	тАт	1111	FILE	205	VUI	110	цу	
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88	Tyr		ьys	Pne	ser	ьуѕ	215	1111	Cys	FIIC	пец	220	OIU	, u _	110	O_Lu	
89		210				ctg		a+ a	222	+ 00	a++		ata	cta	cta	tta	720
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96	Val	тте	Ата	АТа		GIĀ	vaı	TTE	пъ	250	1111	пец	HEC	GIY	255	110	
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99	tgg	דדד	cag	cgg - 3-	gca 1	aay	aty Mot	- Dro	299	ycc • λ1:	LLG LDI	, G1:	ı T.DI	ucc u Th	r Ar	g Gly	010
100	Tr	Pne	e GI	11 AI		а шуз	o Mei	. PIC	26		1 1100	1 01		27	0	5 0-1	
101			~ ~~			+ aa:	a ata	2 200			a aca	r ac	c caa			a aga	864
103	gro	c ago	g CC	y ac	y CC	c Are	y Va	. agg	, 9C , Δ1:	Dra	2 90°	a Th	r Gli	n Gl	n Th	r Arg	
104	٧a.	LAI	9 PI 27		LPI	OMI	y va.	280			J 1110		28	5		5	
105	+ ~ .	~ ~~			a at	+ 40:	a man			a dad	י מאנ	т да			σ σα	g gac	912
107	Lys	aa	y aa a Tii	y ya	n Ta	ι go	a Glu	, guc ı Δer	o Gli	ı Gli	ı Glı	ı Glı	ງ ງ⊆ ປ Asi	n Gli	ı Glı	u Asp	
108	TI	29	_	S AS	ь те	u Arc	29!		01.	. 01.	u 01.	30		- 0-			
109		29	0 ~~	+ ~~	a a+	a 201			T CC	r tad	r att			a cc	t te	t ttc	960
111	acc mb.	ya.	a ya	L 99	u yu	l co	n Dha	Clr	Dr	ጋ	r T14	- G1	ı Pr	o Pr	o Se:	r Phe	
112			u AS	ь ст	y va	310		5 011	1 11	J 17.	31					320	
113	305		~ ~~	2 (72	a a =			- cc	9 00	T Car			a ac	t. aa	t. aa	g gtg	1008
115	CL	999	y Ca	a ya	9 Ca	c Cay	, yς . λ1:	Dr	1 991	y Hie	s Se	r Gl	n Ala	a Gl	v Gl	y Val	
116 117	те	ı Gı	у Ст	11 G1	32		LAT		<i>,</i> 01.	330					33	5	
119	~~.	a +a	- ~~	a 2a			r act	r cct	cto			ааσ	c qa	а от		c tct	1056
120	yaı	0 60	a 99 r Cl	y uy v Ar	g CC a Dr	o Are	η 90°	a Pro	o Lei	ı Va	1 Pro	o Se	r Gl	u Gl	v Se	r Ser	
121	AS	o se	T G7	34		O AL	,	\	34					35			
121	~~	+ +~	a as			a da	າ ລຸດ:	a a a a			саσ	c ac	t at			c tcc	1104
124	ηC λ1.	L LY'	y ya n Ae	n se	r Se	r Aci	o Are	- ∽g\ ISeI	r Tri	o Ala	a Se	r Th	r Va	l As	p Se	r Ser	
124	W.T.	2 II.	р АS 35		- 56	- vol		360					36	5	•		
123			رر	,				500	-								•

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136	Phe	Ser	Lys	Asp		GTĀ	Pne	Leu	GIU	410	теп	PIU	Glu	мър	415	цец	
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    192
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                                  455
     225
         Ser Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp
     226
                                                  475
                              470
     227
         Arg Gly Arg Thr Leu Gly His Tyr Met Ala Arg
                          485
     231 <210> SEQ ID NO: 3
     232 <211> LENGTH: 1473
     233 <212> TYPE: DNA
     234 <213> ORGANISM: Artificial Sequence
     236 <220> FEATURE:
     237 <223> OTHER INFORMATION: Degenerate polynucleotide seuquence of SEQ ID NO:2
W--> 239 <221> NAME/KEY: misc_feature
```

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```
240 <222> LOCATION: (1)...(1473)
     241 <223> OTHER INFORMATION: n = A, T, C or G
W--> 243 <400> 3
          atggenggne engarmgntg gggneenytn ytnytntgyy tnytnearge ngeneenggn
                                                                                   60
W--> 244
          mgnccnmgny tngcnccncc ncaraaygtn acnytnytnw sncaraaytt ywsngtntay
                                                                                  120
W--> 245
          ytnacntggy tnccnggnyt nggnaayccn cargaygtna cntayttygt ngcntaycar
                                                                                  180
          wsnwsnccna cnmgnmgnmg ntggmgngar gtngargart gygcnggnac naargarytn
                                                                                  240
W--> 247
          ytntgywsna tgatgtgyyt naaraarcar gayytntaya ayaarttyaa rggnmgngtn
                                                                                  300
W--> 248
          mgnacngtnw snccnwsnws naarwsnccn tgggtngarw sngartayyt ngaytayytn
                                                                                  360
W--> 249
          ttygargtng arcengence neengtnytn gtnytnaene araengarga rathytnwsn
                                                                                  420
W--> 250
          genaaygena entayearyt neencentgy atgeenceny tnttyytnaa rtaygargtn
                                                                                  480
W--> 251
                                                                                  540
          genttytggg gnggnggnge nggnaenaar aenytnttye engtnaenee neayggnear
W--> 252
          congtnoara thacnytnoa roongongon wsngarcayo aytgyytnws ngonmgnaon
                                                                                  600
W--> 253
          athtayacnt tywsngtncc naartaywsn aarttywsna arccnacntg yttyytnytn
                                                                                  660
W--> 254
                                                                                  720
          gargtneeng argenaaytg ggenttyytn gtnytneenw snytnytnat hytnytnytn
₩--> 255
          gtnathgeng enggnggngt nathtggaar aenytnatgg gnaayeentg gttycarmgn
                                                                                  780
MI--> 256
          genaaratge enmgngenyt ngarytnaen mgnggngtnm gneenaenee nmgngtnmgn
                                                                                  840
  -> 257
                                                                                  900
          geneengena encarearae nmgntggaar aargayytng engargayga rgargargar
₩--> 258
          gaygargarg ayacngarga yggngtnwsn ttycarcent ayathgarce necnwsntty
                                                                                  960
W--> 259
          ytnggncarg arcaycargc nccnggncay wsngargcng gnggngtnga ywsnggnmgn
                                                                                 1020
W--> 260
          conmgngenc enythqtnee nwsngarggn wsnwsngent gggaywsnws ngaymgnwsn
                                                                                 1080
W--> 261
          tgggcnwsna cngtngayws nwsntgggay mgngcnggnw snwsnggnta yytngcngar
                                                                                 1140
W--> 262
          aarggneeng gnearggnee nggnggngay ggneayearg arwsnytnee neencengar
                                                                                 1200
W--> 263
          ttywsnaarg aywsnggntt yytngargar ytnccngarg ayaayytnws nwsntgggcn
                                                                                 1260
W--> 264
                                                                                 1320
          achtqqqqna cnytnccncc ngarccnaay ytngtnccng gnggnccncc ngtnwsnytn
W--> 265
          caracnytna cnttytgytg ggarwsnwsn ccngargarg argargargc nmgngarwsn
                                                                                 1380
W--> 266
          garathgarg aywsngaygc nggnwsntgg ggngcngarw snacncarmg nacngargay
                                                                                 1440
W--> 267
          mgnggnmgna cnytnggnca ytayatggcn mgn
                                                                                 1473
     270 <210> SEQ ID NO: 4
     271 <211> LENGTH: 203
     272 <212> TYPE: PRT
     273 <213> ORGANISM: Homo sapiens
     275 <400> SEQUENCE: 4
          Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu Leu Ser Gln Asn
     276
                                               10
                           5
     277
          Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly Asn Pro Gln Asp
     278
     279
                      20
                                           25
          Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr Arg Arg Arg Trp
     280
                                       40
     281
          Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu Leu Cys Ser Met
     282
     283
          Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe Lys Gly Arg Val
     284
                                                   75
     285
                              70
          Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val Glu Ser Glu Tyr
     286
     287
                                               90
          Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro Val Leu Val Leu
     288
                                           105
     289
                      100
          Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr Tyr Gln Leu Pro
     290
                                       120
                                                            125
     291
                  115
```

RAW SEQUENCE LISTING ERROR SUMMARY PATENT APPLICATION: US/09/995,898A

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Input Set : A:\00-108.txt

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

```
Seq#:3; N Pos. 6,9,12,18,24,27,30,33,36,42,45,51,54,57,60,63,66,69,72,75,78
Seq#:3; N Pos. 81,90,93,96,99,102,114,117,123,126,132,135,138,141,144,150
Seq#:3; N Pos. 159,162,171,174,183,186,189,192,195,198,201,207,213,225,228
Seq#:3; N Pos. 231,240,243,249,261,276,294,297,300,303,306,309,312,315,318
Seq#:3; N Pos. 321,327,330,336,342,351,360,369,375,378,381,384,387,390,393
Seq#:3; N Pos. 396,399,405,417,420,423,429,432,441,444,447,456,459,462,468
Seq#:3; N Pos. 480,483,492,495,498,501,504,507,513,516,522,525,528,531,537
Seq#:3; N Pos. 543,546,555,558,564,567,570,573,588,591,594,597,600,609,615
Seq#:3; N Pos. 618,621,630,639,645,648,657,660,666,669,675,684,690,693,696
Seq#:3; N Pos. 699,702,705,708,714,717,720,723,729,732,735,738,741,753,756
Seq#:3; N Pos. 762,768,780,783,792,795,798,801,807,810,813,816,819,822,825
Seq#:3; N Pos. 828,831,834,837,840,843,846,849,852,861,864,879,882,915,924
Seq#:3; N Pos. 927,930,939,951,954,957,963,966,981,984,987,993,999,1002
Seq#:3; N Pos. 1005,1008,1014,1017,1020,1023,1026,1029,1032,1035,1038,1041
Seq#:3; N Pos. 1044,1050,1053,1056,1059,1068,1071,1077,1080,1086,1089,1092
Seq#:3; N Pos. 1095,1101,1104,1113,1116,1119,1122,1125,1128,1134,1137,1146
Seq#:3; N Pos. 1149,1152,1158,1161,1164,1167,1173,1185,1188,1191,1194,1197
Seq#:3; N Pos. 1206,1215,1218,1224,1233,1236,1248,1251,1254,1260,1263,1269
Seq#:3; N Pos. 1272,1275,1278,1281,1287,1293,1296,1299,1302,1305,1308,1311
Seq#:3; N Pos. 1314,1317,1320,1326,1329,1332,1347,1350,1353,1371,1374,1380
Seq#:3; N Pos. 1395,1401,1404,1407,1413,1416,1422,1425,1431,1434,1443,1446
Seq#:3; N Pos. 1449,1452,1455,1458,1470,1473
Seq#:5; Xaa Pos. 3
Seq#:28; N Pos. 6,9,12,18,24,27,30,33,36,42,45,51,54,57,60,63,66,69,72,75
Seq#:28; N Pos. 78,81,90,93,96,99,102,114,117,123,126,132,135,138,141,144
Seq#:28; N Pos. 150,159,162,171,174,183,186,189,192,195,198,201,207,213,225
Seq#:28; N Pos. 228,231,240,243,249,261,276,294,297,300,303,306,309,312,315
Seq#:28; N Pos. 318,321,327,330,336,342,351,360,369,375,378,381,384,387,390
Seq#:28; N Pos. 393,396,399,405,417,420,423,429,432,441,444,447,456,459,462
Seq#:28; N Pos. 468,480,483,498,501,504,513,516,522,525,528,531,537,543,546
Seq#:28; N Pos. 555,558,564,567,570,573,588,591,594,597,600,609,615,618,621
Seq#:28; N Pos. 630,639,645,648,657,660,666,669,675,684,690,693,696,699,702
Seq#:28; N Pos. 705,708,714,717,720,723,729,732,735,738,741,753,756,762,768
Seq#:28; N Pos. 780,783,792,795,798,801,810,813,819,825,828,831,834,843,846
Seq#:28; N Pos. 849,852,858,861,870,876,882,894,897,900,903,906,909,912,915
\mathtt{Seq\#:28;\ N\ Pos.\ 918,921,924,927,930,933,936,939,948,951,966,969,1002,1011}
Seq#:28; N Pos. 1014,1017,1026,1038,1041,1044,1050,1053,1068,1071,1074,1080
Seq#:28; N Pos. 1086,1089,1092,1095,1101,1104,1107,1110,1113,1116,1119,1122
Seq#:28; N Pos. 1125,1128,1131,1137,1140,1143,1146,1155,1158,1164,1167,1173
Seq#:28; N Pos. 1176,1179,1182,1188,1191,1200,1203,1206,1209,1212,1215,1221
Seq#:28; N Pos. 1224,1233,1236,1239,1245,1248,1251,1254,1260,1272,1275,1278
Seq#:28; N Pos. 1281,1284,1293,1302,1305,1311,1320,1323,1335,1338,1341,1347
Seq#:28; N Pos. 1350,1356,1359,1362,1365,1368,1374,1380,1383,1386,1389,1392
Seq#:28; N Pos. 1395,1398,1401,1404,1407,1413,1416,1419,1434,1437,1440,1458
```



RAW SEQUENCE LISTING ERROR SUMMARY
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Seq#:28; N Pos. 1461,1467,1482,1488,1491,1494,1500,1503,1509,1512,1518,1521
Seq#:28; N Pos. 1530,1533,1536,1539,1542,1545,1557,1560
Seq#:29; N Pos. 6,9,12,18,24,27,30,33,36,42,45,51,54,57,60,63,66,69,72,75
Seq#:29; N Pos. 78,81,90,93,96,99,102,114,117,123,126,132,135,138,141,144
Seq#:29; N Pos. 150,159,162,171,174,183,186,189,192,195,198,201,207,213,225
Seq#:29; N Pos. 228,231,240,243,249,261,276,294,297,300,303,306,309,312,315
Seq#:29; N Pos. 318,321,327,330,336,342,351,360,369,375,378,381,384,387,390
Seq#:29; N Pos. 393,396,399,405,417,420,423,429,432,441,444,447,456,459,462
Seq#:29; N Pos. 468,480,483,498,501,504,513,516,519,522,528,531,534,537,540
Seq#:29; N Pos. 543,546,549,552,558,564,567,570,579,582,585,591,594,597,600
Seq#:29; N Pos. 603,606,609,618,624,627,633
Seq#:34; Xaa Pos. 10